

REMARKS

In accordance with the sequence rules, applicants have enclosed the following:

1. A computer readable form (CRF) copy of the new Sequence Listing in the form of a 3 1/2" diskette;
2. A paper copy of the new Sequence Listing, pages 1-7; and
3. A statement that the content of the paper and computer readable form are the same and include no new matter.

The Sequence Listing has been corrected to be of the proper format, and the specification has been amended to refer to SEQ ID NOs. Since the sequences as presented in the replacement Sequence Listing were presented in the specification as originally filed or in the drawings as originally filed, no new matter is involved. Applicants respectfully request that the Sequence Listing be entered and maintain that the application now complies with the sequence rules.

Respectfully submitted,

Dated: August 20, 2001

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Certificate of Mailing - 37 CFR 1.8(a)	
I hereby certify that this correspondence is being deposited with the United States Postal Service as first class mail in an envelope addressed to: Assistant Commissioner for Patents, Washington, D.C. 20231, on the date below.	
<u>08-20-01</u>	<u>Susan J. Braman</u> Susan J. Braman
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Marked-Up Version of Paragraph(s):

Page 2, lines 8-16:

Figure 4 illustrates the sequence of the TIG-1 cDNA: The deduced open reading frame of the TIG-1 cDNA is shown (SEQ ID NO:1), as well as the amino acid sequence (SEQ ID NO:3) and the full nucleotide sequence (SEQ ID NO:2). Underlined is the putative bipartite nuclear localization signal (SEQ ID NO:4: RRMINKIDKNEDRKK). The three circles underneath TAR represent a putative protein kinase C phosphorylation site. The sequence QSSQAE (SEQ ID NO:5) is a putative casein kinase II phosphorylation site. The filled in bars below the sequences NVSS and NFSV represent potential N-glycosylation sites.

Page 2, lines 17-21:

Figure 5 shows a representation of the amino acid sequence of the TIG-1 protein: The glutamine and serine/proline rich domains are noted. The glutamine rich repeat sequences are shown (SEQ ID NO: 6). The putative nuclear localization signal is shown in black.

Page 15, lines 25-31:

An example of the protein is the protein encoded by the nucleotide sequence as shown in SEQ ID NO:1 (this is the open reading frame). The amino acid sequence encoded by this nucleotide sequence is shown in SEQ ID NO:3. The full nucleotide sequence is as shown in SEQ ID NO:2. [The amino acid sequence encoded by this nucleotide sequence is shown in SEQ ID NO:4.]

Page 30, lines 14-25:

The protocol elaborated by Wang and Brown 1991 with some modification. Long cDNAs were digested with the restriction endonuclease Rsa 1 and then ligated to linker DNAs (SEQ ID NO:7: 5'GAATTCAGATCTCCCGGGTCACCGC3' and SEQ

ID NO:8: 5'TGACCCGGGAGATCGAATTC3'). Linkered cDNA fragments were amplified by PCR. PCR amplified cDNA fragments constructed from the TPA induced mRNAs were used as "tracer" cDNAs, while a five fold molar excess of biotinylated PCR amplified cDNA fragments constructed from hemin induced mRNAs were used as "driver" cDNAs to produce a EST library that was highly enriched in cDNA fragments generated from the TPA induced K562 cells.